

GenCore version 5.1.4-p5-4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:43:18 ; search time 27.9564 seconds  
(1237.942 Million cell updates/sec)

Title: US-09-625-573-4  
Perfect score: 1900  
Sequence: 1 MLSTSRSRFRNTNESGEEV.....DGVTSTNTPSTGEQEVSAGL 360

Scoring table: BLOSUM62  
Gappp 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 2832224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73;\*

1: Pirl;\*

2: Pir3;\*

3: Pir3;\*

4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1900	100.0	360	2	JC2443		chemokine (C-C) receptor
2	1615.5	86.9	374	2	JC2443		chemokine (C-C) receptor
3	1364	71.8	352	2	A43113		chemokine (C-C) receptor
4	1036	54.5	355	2	A45177		chemokine (C-C) receptor
5	1010.5	53.2	359	2	I49341		MIP-1 alpha receptor
6	963.5	50.7	355	2	I49339		macrophage inflammatory protein-1 receptor
7	951	50.1	355	2	G02436		chemokine (C-C) receptor
8	871	45.8	360	2	JC4587		chemokine (C-C) receptor
9	862.5	45.4	360	2	A57160		chemokine (C-C) receptor
10	822.5	43.3	383	2	S55594		G protein-coupled receptor
11	778.5	41.0	356	2	I49340		MIP-1 alpha receptor
12	751	39.5	355	2	JC5067		G protein-coupled receptor
13	722.5	38.0	354	2	I58186		probable G protein receptor
14	708	37.3	355	2	JC4304		orphan G protein-coupled receptor
15	649.5	34.2	344	2	JC5942		chemokine receptor
16	581.5	30.6	378	2	B55735		lymphocyte-specific G protein-coupled receptor
17	569	29.9	378	2	A55735		G protein-coupled receptor
18	567.5	29.9	378	2	A45680		G protein-coupled receptor
19	563	29.6	369	2	JC5068		G protein-coupled receptor
20	547	28.8	360	2	A53611		interleukin-8 receptor
21	540.5	28.4	355	2	J01231		interleukin-8 receptor
22	540.5	28.4	359	2	A48921		interleukin-8 receptor
23	536.5	28.2	358	2	S43752		interleukin-8 receptor
24	532.5	28.0	356	2	S42096		interleukin-8 receptor
25	532	28.0	367	2	JE0349		interferon-inducible G protein-coupled receptor
26	528.5	27.8	333	2	I6598		interleukin-8 receptor fusin (LESTR) - c
27	528.5	27.8	350	2	A39445		neuropeptide Y receptor
28	515.5	27.1	352	2	G00048		MLVVLINCKLKCLDIYLNLAI
29	515.5	27.1	353	2	S28787		MLVVLINCKLKCLDIYLNLAI

## ALIGNMENTS

30	512.5	27.0	352	2	A45747	neuropeptide Y/pep G protein-coupled receptor
31	495.5	26.1	350	2	S10621	angiotensin II receptor
32	486.5	25.6	359	2	S15403	angiotensin II receptor
33	480.5	25.3	359	2	A12656	G protein-coupled receptor
34	480	25.0	374	2	S42628	angiotensin II receptor
35	475.5	25.0	359	2	JC2134	angiotensin II receptor
36	474.5	25.0	359	2	JC1104	angiotensin II receptor
37	474.5	25.0	359	2	J4425	angiotensin II receptor
38	472.5	24.9	359	2	JH0621	angiotensin II receptor
39	471.5	24.8	359	2	JQ1516	angiotensin II receptor
40	469.5	24.7	359	2	JC1194	angiotensin II receptor
41	468.5	24.7	359	2	TS1372	angiotensin II receptor
42	466.6	24.5	359	2	A48857	G protein-coupled receptor
43	465.5	24.5	374	2	S32785	MCRL5, protein - h G protein-coupled receptor
44	465	24.5	327	2	S56162	MCRL5, protein - h G protein-coupled receptor
45	465	24.5	372	2	S26667	

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45	465	24.5	372	2	S26667	

## ALIGNMENTS

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QY 121 HIGYFGGIFTILLTIDYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Db 121 HIGYFGGIFTILLTIDYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

QY 181 CQKEDSVYVCCPYFPGRWNNTIMNLTIMNLLGVLPLIMIVCYSGILKTLRCRNEKKHR 240  
 Db 181 CQKEDSVYVCCPYFPGRWNNTIMNLTIMNLLGVLPLIMIVCYSGILKTLRCRNEKKHR 240

QY 241 AVRVIITIMVYFLFTPTYNVILLNTQEQEGLSNESTSSLDQATQVTEFLGMTHCC1 300  
 Db 241 AVRVIITIMVYFLFTPTYNVILLNTQEQEGLSNESTSSLDQATQVTEFLGMTHCC1 300

QY 301 NPIIYAFVGEKFRRLVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Db 301 NPIIYAFVGEKFRRLVTFGVVTSVITWLVAVFASVPGIIFTK 180

RESULT 3  
 A4.31.13  
 Chemokine (C-C) receptor 5 - human  
 N; Alternate names: C-C CRK-5; CCR5  
 C; Species: Homo sapiens (man)  
 C; Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 20-Jun-2000  
 C; Accession: A4.31.13; S71808; A58834; A58832; G02653; A58833  
 R; Samson, M.; Labbe, O.; Mollerereau, C.; Vassart, G.; Parmentier, M.;  
 Biochemistry 35, 3362-3367, 1996  
 A; Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
 A; Reference number: A43113; MUID: 96241590; PMID: 8639485  
 A; Accession: A43113  
 A; Molecule type: mRNA  
 A; Residues: 1-352 <SAM1>  
 A; Cross-references: GB:X91492; PID: 91262810; PID: 91262811  
 R; Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liensard, C.; Farber, C.M.; Saragovi, H.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Nature 382, 722-725, 1996  
 A; Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant allele  
 A; Reference number: S71808; MUID: 96345670; PMID: 8715444  
 A; Accession: S71808  
 A; Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A; Molecule type: DNA  
 A; Residues: 1-206-207-230 <SAM2>  
 A; Accession: A58834  
 A; Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A; Molecule type: DNA  
 A; Residues: 1-184, IKDSHLGAGPAACGHLLGPNPKNSAVSK/ <SAM3>  
 A; Cross-references: GB:X91393; NID: 91254062; PID: 91254063  
 A; Note: this frameshift mutation results in a non-functional receptor but confers a gain of function by conferring resistance to Yersinia plague infection  
 R; Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M. 1  
 J. Leukoc. Biol. 60, 147-152, 1996  
 A; Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor number: A58832; MUID: 9629570; PMID: 8699119  
 A; Accession: A58832  
 A; Molecule type: mRNA  
 A; Residues: 1-352 <COM1>  
 A; Cross-references: GB:U57840; NID: 91502408; PID: 91502409  
 A; Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
 R; Combadiere, C.  
 A; Reference number: H01541  
 A; Accession: G02653  
 A; Molecule type: mRNA  
 A; Residues: 1-89, L-91-352 <COM2>  
 A; Cross-references: EMBL:057840  
 R; Report, C.J.; Gosling, J.; Schweickart, V.L.; Charo, I.F.  
 J. Biol. Chem. 271, 17161-17166, 1996  
 A; Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor  
 A; Reference number: A58833; MUID: 96291862; PMID: 8663314  
 A; Accession: A58833  
 A; Molecule type: mRNA  
 A; Residues: 1-352 <RAP>  
 A; Cross-references: GB:U54994; NID: 91457945; PID: 91457946  
 C; Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A0574), MIP-1beta and RANTES  
 C; Genes: GDB:CMKBR5; CCR5; CCR-5; CKR5; ChemR13  
 A; Cross-references: GDB:1230510; OMIM: 601373  
 A; Map position: 3p21-3p21  
 C; Function:  
 A; Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES  
 A; Note: probably acts to control granulocyte proliferation and differentiation  
 C; Superfamily: vertebrate rhodopsin phosphoprotein; glycoprotein; phosphoprotein; transmembrane  
 C; Keywords: AIDSe; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane  
 F; 32-56/Domain: transmembrane #status predicted

RESULT 2  
 I38450  
 Chemokine (C-C) receptor 2, splice form A - human  
 C; Species: Homo sapiens (man)  
 C; Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 13-Aug-1999  
 C; Accession: I38450  
 R; Charo, I.F.; Myers, S.J.; Franchi, C.; Connolly, A.J.; Coughlin, S.R.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
 A; Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1  
 A; Reference number: A53477; MUID: 94195821; PMID: 8146186  
 A; Accession: I38450  
 A; Status: Preliminary  
 A; Molecule type: mRNA  
 A; Residues: 1-374 <RBS>  
 A; Cross-references: EMBL:U03882; NID: q472555; PIDN: AAA19119.1; PID: q472556  
 C; Genes: GDB:CMKBR2  
 A; Cross-references: GDB:337364; OMIM: 601267  
 A; Map position: 3p21.3p21  
 C; Superfamily: vertebrate rhodopsin  
 C; Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane  
 F; 4-58/Domain: transmembrane #status predicted <TM1>  
 F; 79-59/Domain: transmembrane #status predicted <TM2>  
 F; 115-136/Domain: transmembrane #status predicted <TM3>  
 F; 154-178/Domain: transmembrane #status predicted <TM4>  
 F; 208-226/Domain: transmembrane #status predicted <TM5>  
 F; 244-265/Domain: transmembrane #status predicted <TM6>  
 F; 292-309/Domain: transmembrane #status predicted <TM7>  
 F; 14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F; 32-277,113-190/Disulfide bonds: #status predicted

Query Match 86.98; Score 1651.5; DB 2; Length 374;  
 Best Local Similarity 95.5%; Pred. No. 5.9e-13; Gaps 3;  
 Matches 319; Conservative 5; Mismatches 5; Indels 7; Gaps 3;

QY 1 MLSTSRSRFINTNSGEVTTFFDYGAPECHKDVKQIGAQLLPPLSVLVEFVGFGVGN 60  
 Db 1 MLSTSRSRFINTNSGEVTTFFDYGAPECHKDVKQIGAQLLPPLSVLVEFVGFGVGN 60

QY 61 MLVLLILINCKLKCDIYUNLAISSLLELITLPLWAHSANNEWFGNACKLFTGLY 120  
 Db 61 MLVLLILINCKLKCDIYUNLAISSLLELITLPLWAHSANNEWFGNACKLFTGLY 120

QY 121 HIGYFGGIFTILLTIDYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 Db 121 HIGYFGGIFTILLTIDYLAIHVAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

QY 181 CQKEDSVYVCCPYFPGRWNNTIMNLTIMNLLGVLPLIMIVCYSGILKTLRCRNEKKHR 240  
 Db 181 CQKEDSVYVCCPYFPGRWNNTIMNLTIMNLLGVLPLIMIVCYSGILKTLRCRNEKKHR 240

QY 241 AVRVIITIMVYFLFTPTYNVILLNTQEQEGLSNESTSSLDQATQVTEFLGMTHCC1 300  
 Db 241 AVRVIITIMVYFLFTPTYNVILLNTQEQEGLSNESTSSLDQATQVTEFLGMTHCC1 300

Query Match 71.8%; Score 1364; DB 2; Length 352;  
 Best Local Similarity 75.5%; Pred. No. 1.6e-108;  
 Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

Qy 24 FDYDY-**G**APCHKD**P**QIGAQ**L**PLP**L**SLVE**T**FGFVG**N**MLV**L**LIN**K**K**C**L**D**IY**L** 81  
 Db 10 YDINYYTSEPCQ**K**LNVK**Q**AA**R**PLP**L**SLVE**T**FGFVG**N**MLV**L**LIN**K**R**L**K**S**M**D**IY**L** 69

Qy 82 LN**L**AS**L**SL**L**FL**L**PL**L**PLW**A**SA**N**EW**V**GN**M**CK**L**FT**G**L**H**IG**R**GG**F**FF**F**LL**T**DRY**L** 141  
 Db 70 LN**L**AS**L**SL**L**FL**L**FL**L**PLW**A**SA**N**EW**V**GN**M**CK**L**FT**G**L**H**IG**R**GG**F**FF**F**LL**T**DRY**L** 129

Qy 142 IV**H**AY**F**AL**K**ART**V**TF**G**V**T**SV**T**W**V**AV**F**AS**P**GL**T**FC**Q**ED**S**V**Y**CP**F** --- RG 197  
 Db 130 IV**H**AY**F**AL**K**ART**V**TF**G**V**T**SV**T**W**V**AV**F**AS**P**GL**T**FC**Q**ED**S**V**Y**CP**F** 189

Qy 198 WNNFT**T**IMRN**L**GLV**L**PL**L**PL**L**IM**C**Y**V**SG**L**IL**T**K**T**LL**R**CR**N**E**K**R**H**AV**R**V**I** 257  
 Db 190 WKNFT**T**IK**T**KV**L**PL**L**PL**L**IM**C**Y**V**SG**L**IL**T**K**T**LL**R**CR**N**E**K**R**H**AV**R**V**I** 249

Qy 258 PY**N**IV**T**L**N**T**Q**EF**F**GL**S**CE**S**T**Q**LD**Q**AT**T**ET**G**M**H**CC**C**IN**I**TY**A**VG**E**K**F**RRY**L** 317  
 Db 250 PY**N**IV**T**L**N**T**Q**EF**F**GL**S**CE**S**T**Q**LD**Q**AT**T**ET**G**M**H**CC**C**IN**I**TY**A**VG**E**K**F**RRY**L** 309

Qy 318 VF**R**K**H**TR**K**RF**C**K**Q**CP**V**FY**R**ET**D**G**V**T**S**T**N**P**G**E**Q**V**S**AG**L** 360  
 Db 310 VF**R**Q**K**HA**K**RF**C**K**C**CS**F**Q**E**AP**R**AS**S**V**T**R**S**GE**T**SV**G**L 352

## RESULT 4

A45177 chemokine (C-C) receptor 1 - human  
 N; Alternate names: C-C CKR1; macrophage inflammatory protein-1-alpha receptor  
 C; Species: Homo sapiens (man)  
 C; Sequence revision: 30-Sep-1993 #text\_change 13-Aug-1999  
 C; Accession: I45177; I55671; R; Note: K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.  
 Cell 72, 415-425, 1993  
 A; Title: Molecular cloning, functional expression and signaling characteristics of a C-  
 A; Reference number: A45177; MUID:93161416; PMID:7679328  
 A; Accession: A45177  
 A; Status: preliminary; translated from GB/EMBL/DBJ  
 A; Molecule type: DNA  
 A; Residues: 1-359 <RES>  
 A; Cross-references: EMBL:U28406; NID:9881551; PID:g881552  
 A; Experimental source: GB:L10918; NID:9292416; PID:9292417  
 A; Note: sequence extracted from NCBI backbone (NCBIP:124876)  
 R; Gao, J.  
 J. Exp. Med. 177, 1421-1427, 1993  
 A; Title: Structure and functional expression of the human macrophage inflammatory 1 alpha  
 A; Reference number: I55671; MUID:93240122; PMID:7683036  
 A; Accession: I55671  
 A; Status: preliminary; translated from GB/EMBL/DBJ  
 A; Molecule type: mRNA  
 A; Residues: 1-355 <RES>  
 A; Cross-references: GB:L10918; NID:9292416; PID:9292417  
 C; Genes: GDB:CMRBR1; CMRBR1  
 A; Cross-references: GDB:138446; OMIM:601159  
 A; Map position: 3p21.3p21  
 C; Superfamily: vertebrate rhodopsin  
 C; Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t-

## RESULT 5

I49341 MIP-1 alpha receptor like-2 - mouse  
 N; Alternate names: C-C CRK2; macrophage inflammatory protein-1-alpha receptor  
 C; Species: Mus musculus (house mouse)  
 C; Date: 02-Jul-1996 #sequence\_change 02-Jul-1998  
 C; Accession: I49341  
 R; Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995  
 A; Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes  
 A; Reference number: I49339; MUID:95340546; PMID:7542241  
 A; Accession: I49341  
 A; Status: preliminary; translated from GB/EMBL/DBJ  
 A; Molecule type: DNA  
 A; Residues: 1-359 <RES>  
 A; Cross-references: EMBL:U28406; NID:9881551; PID:g881552  
 C; Superfamily: vertebrate rhodopsin

Query Match 53.2%; Score 1010.5; DB 2; Length 359;  
 Best Local Similarity 53.5%; Pred. No. 1.9e-78;  
 Matches 193; Conservative 62; Mismatches 81; Indels 25; Gaps 6;

Qy 10 IRNTNESEGEYTFEDYDYGAPCHKD**P**V**K**Q**I**G**A**Q**L**PLP**L**SL**L** 69  
 Db 8 IKTVVSEF-**T**TPYEWEAP**C**VK**I**E**G**SW**L**PLP**L**SL**L** 65

Qy 70 CKK**L**CL**D**IV**L**LN**A**LS**D**LL**F**IT**L**PI**W**HS**A**-NEW**V**GN**M**CK**L**PL**T**GL**H**IG**Y**GG**I** 128  
 Db 66 YRK**Q**IMTN**V**LN**A**LS**D**LL**F**IT**L**PI**W**HS**A**-NEW**V**GN**M**CK**L**SL**G**FX**L**Y**A**SEI 125

Qy 129 FFL**L**IT**D**RY**L**AV**I**RA**V**FA**L**K**T**RT**F**GV**T**SV**T**W**V**AV**S**P**G**LI**F**TC**Q**ED**S**V 188  
 Db 126 FFL**L**IT**D**RY**L**AV**I**RA**V**FA**L**K**T**RT**F**GV**T**SV**T**W**V**AV**S**P**G**LI**F**TC**Q**ED**S**V 185

RESULT 6  
49339  
macrophage inflammatory protein-1 alpha receptor - mouse  
Species: *Mus musculus* (house mouse)  
Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
Accession: I49339  
Murphy, P.M.  
Gao, J.L.  
Biol. Chem. 270, 17494-17501, 1995  
Title: Cloning and differential tissue-specific expression of three mouse  
Reference number: 149339; MUID:95340546; PMID:7542241  
Accession: I49339  
Preliminary; translated from GB/EMBL/DBJ  
Molecule type: DNA  
Residues: 1-355 <RES>  
Cross-references: EMBL:U28404; NIDN:9881547; PIDN:AAA89153.1; PID:9881548  
Superfamily: vertebrate rhodopsin

RESULT 7  
 02436  
 Phenomenine (C-C) receptor 3 - human  
 ; Alternate names: C-C CKR-3  
 ; Species: Homo sapiens (man)  
 ; Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 04-Mar-2000  
 ; Accession: G02436; A57237  
 ; Pionath, P.D.  
 ; Submitted to the EMBL Data Library, February 1996  
 ; Reference number: H01222

A; Accession: G02436  
 A; Status: translated from GB/EMBL/DBJ  
 A; Molecule type: DNA  
 A; Residues: 1-355 <PON>  
 A; Cross references: ENB:U49727; NID:91477560; PIDN:AAB09726.1; PID:91477561  
 A; Cross references: C. I. Alhula, S. K. R. Combadiere, C. J. Murphy, P. M. J. Biol. Chem. 270, 16491-16494, 1995  
 A; Title: Cloning and functional expression of a human eosinophil CC chemokine receptor  
 A; Reference number: A57337; MUID:95348056; PMID:7622448  
 A; Accession: A57337  
 A; Status: nucleic acid sequence not shown  
 A; Molecule type: tRNA  
 A; Residues: 1-106; 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>  
 A; Cross references: GB:U28694; NID:91199579; PIDN:AA0469.1; PID:91199580  
 A; Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN: AAC5  
 C; Genetics:

A: Gene: GDB:CMKBR3	A: Cross-references: GDB:579624 ; OMIM: 601268
A: Map position: 3p21 -3p21	C: Superfamily: vertebrate rhodopsin
C: Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane	F: 36 -60/Domain: transmembrane #status predicted <TM1>
F: 71 -91/Domain: transmembrane #status predicted <TM2>	F: 108 -129/Domain: transmembrane #status predicted <TM3>
F: 147 -171/Domain: transmembrane #status predicted <TM4>	F: 205 -223/Domain: transmembrane #status predicted <TM5>
F: 240 -261/Domain: transmembrane #status predicted <TM6>	F: 288 -305/Domain: transmembrane #status predicted <TM7>
F: 24 -23/1683/Disulfide bonds: #status predicted	F: 345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
Query Match 50.1% ; Score 951 ; DB 2 ; Length 355 ;	Best Local Similarity 52.6% ; Pred. No. 2.1e-73 ;
Matches 180 ; Conservative 65 ; Mismatches 89 ; Indels 8 ; Gaps 5 ;	
Qy 21 TTFFDYDGAPCHFDYKQIGAQOLPPLSVPFTFGFGNMLVYLINCKKRCQLTDY 80	Db 14 TSYYD-DVGLCEKADTRALMAQFVPLPLSVPFTVGQLGNVVWMLIKYRRLIMTNIV 72
Qy 81 LLNLALSDLLFLITPLWAHSA-ANEWYFGNAMCKLFGTGLYHIGYFGGIFTILITDLY 139	Db 73 LLNLALSDLLFLITPLWTHYRGRHNNVFGHGNCKLLEGFYHGLYSEIFFILITDLY 132
Qy 140 LAIVHAVFAKARTWPGVWTSVITWLYAVFASVPGI-LIFTKCOKEDESVVCGPKFPR-- 196	Db 133 LAIVHAVFALRARTVAFGVTSIVTGVLAVLAALPEFLFVETBEEFLCSALAYPEDTV 192
Qy 197 -GWNINHTIMRNILGIVLPLLIMVYCSGILKTLRLCNEKKRRAVRYIFTIMIVYFLF 255	Db 193 YSWRHTLRLMTIVLPLLYMAICYGTIKTLRCPs-KKKYKAIRLIVMAVFFIF 251
Qy 256 WTPYNTVILNNTFQEFFGGLNSCESTSOLDOATQVTTETLGMTHCINPIYAFAVGEKFRKY 315	Db 252 WTPYNAVAILLSSYQSLIFGNDERTKHLVLMTEVIAVSHCCMNPVYAFVGERFRKY 311
Qy 316 LSVFVERKHKITKRCQCPVVFRETVDGYTSTNTPSTGQEOVS 357	Db 312 LRFHFRHLMLHLGRYIPLPSEKLER-TSSVSPSTAPELS 352

chemokine (C-C) receptor 4 - mouse  
 C:Species: *Mus musculus* (house mouse)  
 C:Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000  
 C:Accession: JC587  
 R:Hoogerwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996  
 A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokine  
 A:Reference number: JC45B7; MUID:9616324; PMID:8573157  
 A:Accession: JC587  
 A:Residues: 1-360  
 A:Molecule type: mRNA

A;Cross-references: EMBL:X90862; NID:91167851; PID:CAA62372.1; #status predicted  
C;Experimental source: thymus

A;Gene: cc ckr-4

C;Superfamily: vertebrate rhodopsin

C;Keywords: glycoprotein; phosphoprotein; receptor; thymus

C;Alternate names: C-C ckr-4

C;Species: Homo sapiens (man)

C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000

C;Accession: A57160

R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W

J.; Biol. Chem. 270, 19495-19500, 1995

A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cD

A;Reference number: A57160; MUID:95310289; PMID:7612634

A;Accession: A57160

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-360 <POW>

A;Cross-references: GB:X85740; NID:91370103; PID:CAA59743.1; #status predicted

A;Note: source clone K5-5

C;Genetics:

A;Gene: CMKBR4

A;Cross-references: GDB:677463

A;Map position: 3p21.3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F;40-65/Domain: transmembrane #status predicted <TM1>

F;76-97/Domain: transmembrane #status predicted <TM2>

F;112-133/Domain: transmembrane #status predicted <TM3>

F;151-175/Domain: transmembrane #status predicted <TM4>

F;208-226/Domain: transmembrane #status predicted <TM5>

F;243-264/Domain: transmembrane #status predicted <TM6>

F;291-309/Domain: transmembrane #status predicted <TM7>

F;291-326/110-187/Disulfide bonds: #status predicted

F;72-350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F;183-194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match Score 45.4%; Score 862.5; DB 2; Length 360;  
Best Local Similarity 48.7%; Pred. No. 7.2e-66;  
Matches 164; Conservative 67; Mismatches 95; Indels 11; Gaps 4;

Qy 31 PCKHFDVKOICAQQLPPLSYLVEFVGVLLINCKLCKTDIYLNLALISDIL 90  
Db 28 PCTKEGKAKGELFLPPLSYLVEFVGLGNSSVVLFLKRYKRSMDPVYLNLALISDIL 87

Query Match Score 871; DB 2; Length 360;  
Best Local Similarity 47.5%; Pred. No. 1.4e-66; Mismatches 103; Indels 12; Gaps 5;

Db 88 FVFSLFWGYYAADDQWVFLGKCKMISWMLVGFYSSIFVMMMSIDRYLAIVHAFSLR 147

Qy 100 IRNTNESGEVTTEFFDYD-YGAPCHKFDVKQIGAQLLPPLSYLVEFVGVNLMLVLLI 68  
Db 6 VDTDQDTEVYNSZYSEMPKPCPKTEGKAFGEVFLPPLSYLVEFVGLFGNSVYVVLW 65

Qy 69 NCKLKCKLTDIYLNLALISDILFLVLLIISDILFLVLLIISDILFLVLLIISDILFLVLLI 128  
Db 66 KYKRLKSMSTDYLNLALISDILFLVLLIISDILFLVLLIISDILFLVLLIISDILFLVLLI 125

Qy 129 FFLILITIDRYLAIVHAFALKARTVYFGVYTSVITWLWAVYASVPGFLIFTKQKEDSVY 188  
Db 126 FFIMLMSIDRYLAIVHAFSLKARTLYGVITSLWAVAEASLPGFLSTCYTEHNHT 185

Qy 189 VCGPYF - -PRGWNNEHTIMRNIGLYPLPLIMIVCYSGILKTLRORNEKKRHRAVRVI 245  
Db 186 YCKTQYSVNSTTWKVLSSLEINVNLGLLIPQKMLFNYSMISIRTLQHCKNEK - NRAVMI 244

Qy 246 FTIMIVYFLFWTQVITLNLNTQFQEFFGLQESTSDQATQVITLGMTHCCINPLTY 305  
Db 245 FGVVVFLGFFTPVNVLFLTLEVLEVQDCTLERYDYAQATEFLGFHCCLNPIYY 304

Qy 306 AFYGEKFRYLSVFFRKHITKR---FCKQCPFYRETVDGTYSTNTNPSTGQE 355  
Db 305 FFLGERKFRYLTQFLFR---TCRGPLVCKHCDLFLQVYSADMSSSTQSTVHD 355

RESULT 9

A57160 chemokine (C-C) receptor 4 - human  
C;Species: Homo sapiens (man)  
C;Accession: A57160  
C;Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W

J.; Biol. Chem. 270, 19495-19500, 1995

A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cD

A;Reference number: A57160; MUID:95310289; PMID:7612634

A;Accession: A57160

A;Molecule type: mRNA

A;Residues: 1-360 <POW>

A;Cross-references: GB:X85740; NID:91370103; PID:CAA59743.1; #status predicted

A;Note: source clone K5-5

C;Genetics:

A;Gene: GDB:CMKBR4

A;Cross-references: GDB:677463

A;Map position: 3p21.3p21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F;40-65/Domain: transmembrane #status predicted <TM1>

F;76-97/Domain: transmembrane #status predicted <TM2>

F;112-133/Domain: transmembrane #status predicted <TM3>

F;151-175/Domain: transmembrane #status predicted <TM4>

F;208-226/Domain: transmembrane #status predicted <TM5>

F;243-264/Domain: transmembrane #status predicted <TM6>

F;291-309/Domain: transmembrane #status predicted <TM7>

F;291-326/110-187/Disulfide bonds: #status predicted

F;72-350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match Score 45.4%; Score 862.5; DB 2; Length 360;  
Best Local Similarity 48.7%; Pred. No. 7.2e-66;  
Matches 164; Conservative 67; Mismatches 95; Indels 11; Gaps 4;

Qy 31 PCKHFDVKOICAQQLPPLSYLVEFVGVLLINCKLCKTDIYLNLALISDIL 90  
Db 28 PCTKEGKAKGELFLPPLSYLVEFVGLGNSSVVLFLKRYKRSMDPVYLNLALISDIL 87

Query Match Score 871; DB 2; Length 360;  
Best Local Similarity 47.5%; Pred. No. 1.4e-66; Mismatches 103; Indels 12; Gaps 5;

Db 88 FVFSLFWGYYAADDQWVFLGKCKMISWMLVGFYSSIFVMMMSIDRYLAIVHAFSLR 147

Qy 100 IRNTNESGEVTTEFFDYD-YGAPCHKFDVKQIGAQLLPPLSYLVEFVGVNLMLVLLI 68  
Db 6 VDTDQDTEVYNSZYSEMPKPCPKTEGKAFGEVFLPPLSYLVEFVGLFGNSVYVVLW 65

Qy 69 NCKLKCKLTDIYLNLALISDILFLVLLIISDILFLVLLIISDILFLVLLIISDILFLVLLI 128  
Db 66 KYKRLKSMSTDYLNLALISDILFLVLLIISDILFLVLLIISDILFLVLLIISDILFLVLLI 125

Qy 129 FFLILITIDRYLAIVHAFALKARTVYFGVYTSVITWLWAVYASVPGFLIFTKQKEDSVY 188  
Db 126 FFIMLMSIDRYLAIVHAFSLKARTLYGVITSLWAVAEASLPGFLSTCYTEHNHT 185

Qy 189 VCGPYF - -PRGWNNEHTIMRNIGLYPLPLIMIVCYSGILKTLRORNEKKRHRAVRVI 245  
Db 186 YCKTQYSVNSTTWKVLSSLEINVNLGLLIPQKMLFNYSMISIRTLQHCKNEK - NRAVMI 244

Qy 246 FTIMIVYFLFWTQVITLNLNTQFQEFFGLQESTSDQATQVITLGMTHCCINPLTY 305  
Db 245 FGVVVFLGFFTPVNVLFLTLEVLEVQDCTLERYDYAQATEFLGFHCCLNPIYY 304

Qy 306 AFYGEKFRYLSVFFRKHITKR---FCKQCPFYRETVDGTYSTNTNPSTGQE 355  
Db 305 FFLGERKFRYLTQFLFR---TCRGPLVCKHCDLFLQVYSADMSSSTQSTVHD 355

RESULT 10

S55594

G;protein-coupled receptor El - equine herpesvirus 2  
C;Species: equine herpesvirus 2  
C;Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 13-Aug-1999  
C;Accession: S55594  
R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-526, 1995  
A;Title: The DNA sequence of equine herpesvirus 2  
A;Reference: GB:U20824; NID:9695172; PMID:95302501;  
A;Accession: S55594  
A;Molecule type: DNA  
A;Status: preliminary; nucleic acid sequence not shown  
A;Cross-references: GB:U20824; NID:9695172; PMID:95302501;  
A;Keywords: G protein-coupled receptor

Query Match Score 43.3%; Score 822.5; DB 2; Length 383;  
Best Local Similarity 47.9%; Pred. No. 1.9e-62;  
Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;

Qy 4 TSSRSRFRINNESEGEVTTFFEDDYD - GAPHKFDVKQIGAQLLPPLSYLVEFVGVNM 61  
Db 32 TTAISAPSYSDYYDDQDYEESAPVYKSDTTRIAQVPAVYVPLVYVFLFGJLGN 91

Qy 62 LVLVLLINCKLCKTDIYLNLALISDILFLVLLIISDILFLVLLIISDILFLVLLI 119  
Db 92 LVLVLLVRYMKINLTNMNLNLALISDILFLVLLIISDILFLVLLIISDILFLVLLI 151

Qy 120 YHIGYFGGIGFLITLITIDRYLAIVHAFALKARTVYFGVYTSVITWLWAVASVPGFLFT 179  
Db 152 CYMSLYSQVFCILITVDRYAVVYAVTALRFTVCGIVTCVTFWAGLISLSPPEFFH 211

Qy 180 KCQEDSVVYCGPYFP---RGWNNFHTIMRNIGLYPLPLIMIVCYSGILKTLRORNE 235  
Db 212 GHODNGRVOCDPYPPMSYNNWRRAVKYLMLSLPLUIMAVCYVILRLLRGP 270

Qy 236 KKRHRAVVIFTIMIVYFLFNTPYVNVLNTNTQFEGFLGSNQCTQVTTETLGM 295  
Db 271 KKKYKAIRLIVVIMAYFVWTPNIVLLESTPHATLNLQCALSSNMDMALLTRKTVAY 330



Best Local Similarity	46.28;	Pred.	No. 5.7e-54;	Indels	19;	Gaps	8;	Db	126 DRYLAVLAANSMMNRTVQHGYTISLGWAAAILVAAPQFMFTK-QKENE--CLGDPY 181
Matches	160;	Conservative	46;	Mismatches	121;			Qy	197 GWNNEHTIMRN-----LGLVPLPLIMIVCYSGILKTLRLCRNEKKHRRAVVFITIMIVY 252
Qy	24 FDYDGA-PCHKEDVKIGQLPLPSLVIERGVGNMVLLINCKLKCLETIYLL 82							Db	182 VLEIWWAVLRRNVENTNFQGFLPLIMIVCYFRITQTSCKNHKA-KAIKLLVVTVF 240
Db	13 FEYDSSAECYLGDIVAFTFLSIFYSLVTFGLVNLVLLVLAUTNSRKSLSITIYLL 72							Qy	253 FLWTPNIVLNTFOEFFLNSCSTSOLDQATOVTETLGWTHCCINPLIYAFGEKF 312
Qy	83 NLAISDLFLTTLPLWAHSAAANEWVGNAMECKLFTGLYHTGTFGLVNLVLLVLAUTNSRKSLSITIYLL 72							Db	241 FLWTPNVMFELTUKLYDFFPSCDMRKDURALSYTEAFLSHCCLNPLIYAFGEKF 300
Db	73 NLAISDLFLTTLPLWAHSAAANEWVGNAMECKLFTGLYHTGTFGLVNLVLLVLAUTNSRKSLSITIYLL 142							Qy	313 RRYLYSVERK 322
Qy	143 VHAVFALKARIVTGFVTVTSVTVLWAFASVPGIIFTKCOEDSVVYCCPYFPRGNWNFH 202							Db	301 RRYLYHLYGK- 310
Db	133 VLAANSMMNRTVQHGYTISLGWAAAILVAAPQFMFTK-RKDNE--CLGDPYPEVLEIW 188								
	RESULT 15								
	Qy	203 TIMR---NLLGIVPLPLIMIVCYSGILKTLRLCRNEKKHRRAVVFITIMIVYFLWTP 258						Qy	197 GJ5942
Db	189 PVLRNSEVNLLGIVPLPLIMIVCYSGILKTLRLCRNEKKHRRAVVFITIMIVYFLWTP 247							C;Species: Homo sapiens (man)	chemokine receptor - human
Qy	259 YNIVVLLNTFOEFFLNSCSTSOLDQATOVTETLGWTHCCINPLIYAFGEKFRRYLRH 318							C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999	#text_change 21-Jul-2000
Db	248 YNIVVLETLKFNFPSCGMKDRLRLWALSVTETAFSHCCLNPFTYAFAGEKFRRYLRH 307							C;Accession: JC5942	
Qy	319 FFRKHITKRECKQCPVF-----YRTVDGVTSTNTPSTGEQEVY 357							R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.	
Db	308 LYNKCLAV-LGGR-PVAGFSTESORSRQDSISSLTHYTHSEGEVS 351							A;Title: Cloning and characterization of a novel human chemokine receptor.	
								A;Reference number: JC5942; MUID:98139902;	PMID:9473515
								A;Accession: JC5942	
								A;Status: Preliminary	
								A;Molecule type: DNA	
								A;Residues: 1-344 <FAN>	
								A;Cross-references: GB:U97123; NID:92897070; PID: AAC39595.1; PID:92897071	
								C;Superfamily: Vertebrate rhodopsin	
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
	Query Match	34.28;	Score	649.5;	DB	2;	Length	344;	
	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
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	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;					
	Matches	128;	Indels	17;	Gaps	5;			
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	Matches	128;	Indels	17;	Gaps	5;			
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	Matches	128;	Indels	17;	Gaps	5;			
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	Best Local Similarity	43.08;	Pred.	No. 8.9e-48;		</			

